SEQUENZPROTOKOLL

<110> Deutsches Krebsforschungszentrum

<120> Selektion von monoklonalen Antikörpern

<130> K 2779

<140> PCT/DEOO/00079
<141> 2000-01-11

<150> DE 199 00 635.0-41
<151> 1999-01-11

<160> 6

<170> PatentIn Ver. 2.1.

<210> 1
<211> 5732
<212> DNA
<213> künstliche Sequenz

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<221> CDS
<222> (737) ... (1420)
<223> Beschreibung der künstlichen Sequenz: Antikörper-Bindeprotein

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gaccgcccaa cgacccccgc ccattgacgt caataatgac gtatgttccc atagtaacgc   180

caatagggac tttccattga cgtcaatggg tggactattt acggtaaact gcccacttgg   240

cagtacatca agtgtatcat atgccaagta cgccccctat tgacgtcaat gacggtaaat   300

ggcccgcctg gcattatgcc cagtacatga ccttatggga ctttcctact tggcagtaca   360

tctacgtatt agtcatcgct attaccatgg tgatgcggtt ttggcagtac atcaatgggc   420

gtggatagcg gtttgactca cggggatttc caagtctcca ccccattgac gtcaatggga   480

gtttgttttg gcaccaaaat caacgggact ttccaaaatg tcgtaacaac tccgccccat   540

tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta tataagcaga gctctctggc   600

taactagaga acccactgct tactggctta tcgaaattaa tacgactcac tatagggaga   660

cccaagcttg gtaccgagct cggatccact agtaacggcc gccagtgtgc tggaattcgg   720

cttggggata tccacc atg gag aca gac aca ctc ctg cta tgg gta ctg   769
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                     1   5   10

ctg ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca   817

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Leu Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro
            15              20              25

gat tat gct ggg gcc caa aag ccc gag gtg atc gat gcc agc gag ctg      865
Asp Tyr Ala Gly Ala Gln Lys Pro Glu Val Ile Asp Ala Ser Glu Leu
        30              35              40

acc ccc gcc gtg acc acc tac aag cta gtg atc aac ggc aag acc ctg      913
Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu
    45              50              55

aag ggc gag acc acc acc gag gcc gtg gac gcc gcc acc gcg gag aag      961
Lys Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys
60              65              70              75

gtg ttc aaa caa tac gct aat gac aac ggg gtc gac ggc gag tgg act     1009
Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr
            80              85              90

tac gac gac gcc acc aag acc ttc acc gtg acc gag aag ccc gag gtg     1057
Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val
            95              100             105

atc gat gcc agc gag ctg acc ccc gcc gtg acc acc tac aag cta gtg     1105
Ile Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val
        110             115             120

atc aac ggc aag acc ctg aag ggc gag acc acc acc gag gcc gtg gac     1153
Ile Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Glu Ala Val Asp
    125             130             135

gcc gcc acc gcg gag aag gtg ttc aaa caa tac gct aat gac aac ggg     1201
Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly
140             145             150             155

gtc gac ggc gag tgg act tac gac gac gcc acc aag acc ttc acc gtg     1249
Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val
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acc gag gcg gcc gca gaa caa aaa ctc atc tca gaa gag gat ctg aat      1297
Thr Glu Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
        175             180             185

ggg gcc gtc gac gga caa aac gac acc agc caa acc agc agc ccc tca     1345
Gly Ala Val Asp Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
        190             195             200

gca tcc agc aac ata agc gga ggc att ttc ctt ttc ttc gtg gcc aat     1393
Ala Ser Ser Asn Ile Ser Gly Gly Ile Phe Leu Phe Phe Val Ala Asn
    205             210             215

gcc ata atc cac ctc ttc tgc ttc agt tgaggtgaca cgtctagagc           1440
Ala Ile Ile His Leu Phe Cys Phe Ser
220             225

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<223> Beschreibung der künstlichen Sequenz: Antikörper-Bindeprotein

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Gln Lys Pro Glu Val Ile Asp Ala Ser Glu Leu Thr Pro Ala Val Thr
            35              40                  45

Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr
         50              55                  60

Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr
65               70                  75                  80

Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr
                85                  90                  95

Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala Ser Glu
            100             105                 110

Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr
         115             120                 125

Leu Lys Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu
        130             135                 140

Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp
145             150                 155                 160

Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Ala Ala Ala
                165             170                 175

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Val Asp Gly
            180             185                 190

Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser Ala Ser Ser Asn Ile
            195             200                 205

Ser Gly Gly Ile Phe Leu Phe Phe Val Ala Asn Ala Ile Ile His Leu
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Phe Cys Phe Ser
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<223> Beschreibung der künstlichen Sequenz: Antikörper-Bindeprotein

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cagtacatca agtgtatcat atgccaagta cgccccctat tgacgtcaat gacggtaaat       300

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tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta taagcagag ctctctggc        600

taactagaga acccactgct tactggctta tcgaaattaa tacgactcac tatagggaga       660

cccaagcttg gtaccggtgc g atg gca ccc tgc atg ctg ctc ctg ctg ttg        711
                         Met Ala Pro Cys Met Leu Leu Leu Leu Leu
                          1           5                    10


gcg gcc gcc ctg gcc ccg act cag acc cgc gcg ggg gcc caa aag gag       759
Ala Ala Ala Leu Ala Pro Thr Gln Thr Arg Ala Gly Ala Gln Lys Glu
            15              20              25


aag acc ccc gag gag ccc aag gag gag gtg acc atc aag gcc aac ctg       807
Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu
            30              35              40


atc tac gcc gac ggc aag acc cag acc gcc gag ttc aag ggc acc ttc       855
Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe
            45              50              55


gag gag gcc acc gcg gag gcc tac cgc tac gcc gac gcc ctg aag aag       903
Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys
        60              65              70


gac aac ggc gag tac acc gtg gac gtg gcc gac aag ggc tac acc ctg       951
Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu
75              80              85              90
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aac atc aag ttc gcc ggc aag gag aag acc ccc gag gag ccc aag gag        999
Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu
                95                      100                 105

gag gtg acc atc aag gcc aac ctg atc tac gcc gac ggc aag acc cag       1047
Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln
            110                     115                 120

acc gcc gag ttc aag ggc acc ttc gag gag gcc acc gcg gag gcc tac       1095
Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr
        125                     130                 135

cgc tac gcc gac gcc ctg aag aag gac aac ggc gag tac acc gtg gac       1143
Arg Tyr Ala Asp Ala Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp
        140                 145                 150

gtg gcc gac aag ggc tac acc ctg aac atc aag ttc gcc ggc aag gag       1191
Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu
155                 160                     165                 170

aag acc ccc gag gag ccc aag gag gag gtg acc atc aag gcc aac ctg       1239
Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu
                175                     180                 185

atc tac gcc gac ggc aag acc cag acc gcc gag ttc aag ggc acc ttc       1287
Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe
            190                     195                 200

gag gag gcc acc gcg gag gcc tac cgc tac gcc gac gcc ctg aag aag       1335
Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys
            205                     210                 215

gac aac ggc gag tac acc gtg gac gtg gcc gac aag ggc tac acc ctg       1383
Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu
        220                     225                 230

aac atc aag ttc gcc ggc aag gag aag acc ccc gag gag ccc aag gag       1431
Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu
235                 240                     245                 250

gag gtg acc atc aag gcc aac ctg atc tac gcc gac ggc aag acc cag       1479
Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln
                255                     260                 265

acc gcc gag ttc aag ggc acc ttc gag gag gcc acc gcg gag gcc tac       1527
Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr
                270                     275                 280

cgc tac gcc gac gcc ctg aag aag gac aac ggc gag tac acc gtg gac       1575
Arg Tyr Ala Asp Ala Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp
            285                     290                 295

gtg gcc gac aag ggc tac acc ctg aac atc aag ttc gcc ggc gcg gcc       1623
Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Ala Ala
        300                     305                 310

gca gaa caa aaa ctc atc tca gaa gag gat ctg aat ggg gcc gtc gac       1671
Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Val Asp
315                     320                 325                 330
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gga caa aac gac acc agc caa acc agc agc ccc tca gca tcc agc aac    1719
Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser Ala Ser Ser Asn
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ata agc gga ggc att ttc ctt ttc ttc gtg gcc aat gcc ata atc cac    1767
Ile Ser Gly Gly Ile Phe Leu Phe Phe Val Ala Asn Ala Ile Ile His
            350                 355                 360

ctc ttc tgc ttc agt tgaggtgaca cgtctagagc tattctatag tgtcacctaa    1822
Leu Phe Cys Phe Ser
            365

atgctagagc tcgctgatca gcctcgactg tgccttctag ttgccagcca tctgttgttt    1882

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aaaatgagga aattgcatcg cattgtctga gtaggtgtca ttctattctg gggggtgggg    2002

tggggcagga cagcaagggg gaggattggg aagacaatag caggcatgct ggggatgcgg    2062

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tctttgcaaa agcctaggcc tccaaaaaag cctcctcact acttctggaa tagctcagag    4282

gccgaggagg cggcctcggc ctctgcataa ataaaaaaaa ttagtcagcc atggggcgga    4342

gaatgggcgg aactgggcgg agttaggggc gggatgggcg gagttagggg cgggactatg    4402

gttgctgact aattgagatg catgctttgc atacttctgc ctgctgggga gcctggggac    4462

tttccacacc tggttgctga ctaattgaga tgcatgcttt gcatacttct gcctgctggg    4522

gagcctgggg actttccaca ccctaactga cacacattcc acagctggtt ctttccgcct    4582

caggactctt ccttttcaa taaatcaatc taaagtatat atgagtaaac ttggtctgac    4642

agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt tcgttcatcc    4702

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cccagtgctg caatgatacc gcgagaccca cgctcaccgg ctccagattt atcagcaata    4822

aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc cgcctccatc    4882

cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa tagtttgcgc    4942

aacgttgttg ccattgctac aggcatcgtg gtgtcacgct cgtcgtttgg tatggcttca    5002

ttcagctccg gttcccaacg atcaaggcga gttacatgat cccccatgtt gtgcaaaaaa    5062

gcggttagct ccttcggtcc tccgatcgtt gtcagaagta agttggccgc agtgttatca    5122

ctcatggtta tggcagcact gcataattct cttactgtca tgccatccgt aagatgcttt    5182

tctgtgactg gtgagtactc aaccaagtca ttctgagaat agtgtatgcg gcgaccgagt    5242
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tccagttcga tgtaacccac tcgtgcaccc aactgatctt cagcatcttt tactttcacc    5422

agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg aataagggcg    5482

acacggaaat gttgaatact catactcttc cttttttcaat attattgaag catttatcag    5542

ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa acaaataggg    5602

gttccgcgca catttccccg aaaagtgcca cctgacgcgc cctgtagcgg cgcattaagc    5662

gcggcgggtg tggtggttac gcgcagcgtg accgctacac ttgccagcgc cctagcgccc    5722

gctcctttcg ctttcttccc ttcctttctc gccacgttcg ccggctttcc ccgtcaagct    5782

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cctttgacgt tggagtccac gttctttaat agtggactct tgttccaaac tggaacaaca    5962

ctcaaccctta tctcggtcta ttcttttgat ttataaggga ttttgccgat ttcggcctat    6022

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cttacaattt ac                                                        6094


<210> 4
<211> 367
<212> PRT
<213> künstliche Sequenz
<223> Beschreibung der künstlichen Sequenz: Antikörper-Bindeprotein

<400> 4


Met Ala Pro Cys Met Leu Leu Leu Leu Leu Ala Ala Ala Leu Ala Pro
 1               5                   10                  15

Thr Gln Thr Arg Ala Gly Ala Gln Lys Glu Lys Thr Pro Glu Glu Pro
            20                  25                  30

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
        35                  40                  45

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
    50                  55                  60

Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp Asn Gly Glu Tyr Thr
65                  70                  75                  80

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
                85                  90                  95

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
            100                 105                 110
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Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
            115   120   125

Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
        130   135   140

Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
145   150   155   160

Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
                165   170   175

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
            180   185   190

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
            195   200   205

Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp Asn Gly Glu Tyr Thr
    210   215   220

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
225   230   235   240

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
                245   250   255

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
                260   265   270

Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
        275   280   285

Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
    290   295   300

Thr Leu Asn Ile Lys Phe Ala Gly Ala Ala Ala Glu Gln Lys Leu Ile
305   310   315   320

Ser Glu Glu Asp Leu Asn Gly Ala Val Asp Gly Gln Asn Asp Thr Ser
            325   330   335
Gln Thr Ser Ser Pro Ser Ala Ser Ser Asn Ile Ser Gly Gly Ile Phe
            340   345   350

Leu Phe Phe Val Ala Asn Ala Ile Ile His Leu Phe Cys Phe Ser
            355   360   365

<210> 5
<211> 5729
<212> DNA
<213> künstliche Sequenz

<220>
<221> CDS
<222> (682) ... (1431)
<223> Beschreibung der künstlichen Sequenz: Antikörper-Bindeprotein

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gaccgcccaa cgacccccgc ccattgacgt caataatgac gtatgttccc atagtaacgc    180

caatagggac tttccattga cgtcaatggg tggactattt acggtaaact gcccacttgg    240

cagtacatca agtgtatcat atgccaagta cgccccctat tgacgtcaat gacggtaaat    300

ggcccgcctg gcattatgcc cagtacatga ccttatggga ctttcctact tggcagtaca    360

tctacgtatt agtcatcgct attaccatgg tgatgcggtt ttggcagtac atcaatgggc    420

gtggatagcg gtttgactca cggggatttc caagtctcca ccccattgac gtcaatggga    480

gtttgttttg gcaccaaaat caacgggact ttccaaaatg tcgtaacaac tccgccccat    540

tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta taagcagag ctctctggc     600

taactagaga acccactgct tactggctta tcgaaattaa tacgactcac tataggagga    660

cccaagcttg gtaccggtgc g atg gca ccc tgc atg ctg ctc ctg ctg ttg    711
                         Met Ala Pro Cys Met Leu Leu Leu Leu Leu
                         1               5                   10

gcg gcc gcc ctg gcc ccg act cag acc cgc gcg ggg gcc caa aag ccc    759
Ala Ala Ala Leu Ala Pro Thr Gln Thr Arg Ala Gly Ala Gln Lys Pro
                15                  20                  25

gag gtg atc gat gcc agc gag ctg acc ccc gcc gtg acc acc tac aag    807
Glu Val Ile Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys
            30                  35                  40

cta gtg atc aac ggc aag acc ctg aag ggc gag acc acc acc gag gcc    855
Leu Val Ile Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Glu Ala
            45                  50                  55

gtg gac gcc gcc acc gcg gag aag gtg ttc aaa caa tac gct aat gac    903
Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn Asp
        60                  65                  70

aac ggg gtc gac ggc gag tgg act tac gac gac gcc acc aag acc ttc    951
Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe
75                  80                  85                  90

acc gtg acc gag aag ccc gag gtg atc gat gcc agc gag ctg acc ccc    999
Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala Ser Glu Leu Thr Pro
                95                  100                 105

gcc gtg acc acc tac aag cta gtg atc aac ggc aag acc ctg aag ggc    1047
Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu Lys Gly
                110                 115                 120

gag acc acc acc gag gcc gtg gac gcc gcc acc gcg gag aag gtg ttc    1095
Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe
            125                 130                 135

aaa caa tac gct aat gac aac ggg gtc gac ggc gag tgg act tac gac    1143
Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp
    140                 145                 150

gac gcc acc aag acc ttc acc gtg acc gag gcg gcc gca gaa caa aaa    1191
Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Ala Ala Ala Glu Gln Lys
155                 160                 165                 170
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ctc atc tca gaa gag gat ctg aat ggg gcc gtc gac gaa caa aaa ctc    1239
Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Val Asp Glu Gln Lys Leu
            175                 180                 185

atc tca gaa gag gat ctg aat gct gtg ggc cag gac acg cag gag gtc    1287
Ile Ser Glu Glu Asp Leu Asn Ala Val Gly Gln Asp Thr Gln Glu Val
            190                 195                 200

atc gtg gtg cca cac tcc ttg ccc ttt aag gtg gtg gtg atc tca gcc    1335
Ile Val Val Pro His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala
    205                 210                 215

atc ctg gcc ctg gtg gtg ctc acc atc atc tcc ctt atc atc ctc atc    1383
Ile Leu Ala Leu Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile
    220                 225                 230

atg ctt tgg cag aag aag cca cgt tcg tcg gcc gat cga gaa tcc atc    1431
Met Leu Trp Gln Lys Lys Pro Arg Ser Ser Ala Asp Arg Glu Ser Ile
235             240                 245                 250

tagagctatt ctatagtgtc acctaaatgc tagagctcgc tgatcagcct cgactgtgcc    1491

ttctagttgc cagccatctg ttgtttgccc ctcccccgtg ccttccttga ccctggaagg    1551

tgccactccc actgtccttt cctaataaaa tgaggaaatt gcatcgcatt gtctgagtag    1611

gtgtcattct attctggggg gtggggtggg gcaggacagc aaggggagg attgggaaga    1671

caatagcagg catgctgggg atgcggtggg ctctatggct tctgaggcgg aaagaaccag    1731

tggcggtaat acggttatcc acagaatcag gggataacgc aggaaagaac atgtgagcaa    1791

aaggccagca aaaggccagg aaccgtaaaa aggccgcgtt gctggcgttt ttccataggc    1851

tccgccccc tgacgagcat cacaaaaatc gacgctcaag tcagaggtgg cgaaacccga    1911

caggactata aagataccag gcgtttcccc ctggaagctc cctcgtgcgc tctcctgttc    1971

cgaccctgcc gcttaccgga tacctgtccg cctttctccc ttcgggaagc gtggcgcttt    2031

ctcatagctc acgctgtagg tatctcagtt cggtgtaggt cgttcgctcc aagctgggct    2091

gtgtgcacga accccccgtt cagcccgacc gctgcgcctt atccggtaac tatcgtcttg    2151

agtccaaccc ggtaagacac gacttatcgc cactggcagc agccactggt aacaggatta    2211

gcagagcgag gtatgtaggc ggtgctacag agttcttgaa gtggtggcct aactacggct    2271

acactagaag gacagtattt ggtatctgcg ctctgctgaa gccagttacc ttcggaaaaa    2331

gagttggtag ctcttgatcc ggcaaacaaa ccaccgctgg tagcggtggt ttttttgttt    2391

gcaagcagca gattacgcgc agaaaaaaag gatctcaaga agatcctttg atcttttcta    2451

cggggtctga cgctcagtgg aacgaaaact cacgttaagg gattttggtc atgagattat    2511

caaaaaggat cttcacctag atccttttaa attaaaaatg aagttttaaa tcaatctaaa    2571

gtatatatga gtaacctgag gctatggcag ggcctgccgc cccgacgttg gctgcgagcc    2631

ctgggccttc acccgaactt ggggggtggg gtggggaaaa ggaagaaacg cggcgtatt    2691
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ggccccaatg gggtctcggt ggggtatcga cagagtgcca gccctgggac cgaaccccgc   2751

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cgcgggttcc ttccggtatt gtctccttcc gtgtttcagt tagcctcccc ctagggtggg   2871

cgaagaactc cagcatgaga tccccgcgct ggaggatcat ccagccggcg tcccggaaaa   2931

cgattccgaa gcccaacctt tcatagaagg cggcggtgga atcgaaatct cgtgatggca   2991

ggttgggcgt cgcttggtcg gtcatttcga accccagagt cccgctcaga agaactcgtc   3051

aagaaggcga tagaaggcga tgcgctgcga atcgggagcg gcgataccgt aaagcacgag   3111

gaagcggtca gcccattcgc cgccaagctc ttcagcaata tcacgggtag ccaacgctat   3171

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cctctccacc caagcggccg gagaacctgc gtgcaatcca tcttgttcaa tcatgcgaaa   3831

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ctcactactt ctggaatagc tcagaggccg aggaggcggc ctcggcctct gcataaataa   3951

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cagcgatctg tctatttcgt tcatccatag ttgcctgact ccccgtcgtg tagataacta   4371

cgatacggga gggcttacca tctggcccca gtgctgcaat gataccgcga gacccacgct   4431

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gtagttcgcc agttaatagt ttgcgcaacg ttgttgccat tgctacaggc atcgtggtgt   4611
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cacgctcgtc gtttggtatg gcttcattca gctccggttc ccaacgatca aggcgagtta    4671

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gaagtaagtt ggccgcagtg ttatcactca tggttatggc agcactgcat aattctctta    4791

ctgtcatgcc atccgtaaga tgcttttctg tgactggtga gtactcaacc aagtcattct    4851

gagaatagtg tatgcggcga ccgagttgct cttgcccggc gtcaatacgg gataataccg    4911

cgccacatag cagaacttta aaagtgctca tcattggaaa acgttcttcg gggcgaaaac    4971

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catcgccctg atagacggtt tttcgccctt tgacgttgga gtccacgttc tttaatagtg    5571

gactcttgtt ccaaactgga acaacactca accctatctc ggtctattct tttgatttat    5631

aagggatttt gccgatttcg gcctattggt taaaaaatga gctgatttaa caaaaattta    5691

acgcgaattt taacaaaata ttaacgctta caatttac                            5729
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<210> 6
<211> 250
<212> PRT
<213> künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz: Antikörper-Bindeprotein

<400> 6

Met Ala Pro Cys Met Leu Leu Leu Leu Leu Ala Ala Ala Leu Ala Pro
1   5   10   15

Thr Gln Thr Arg Ala Gly Ala Gln Lys Pro Glu Val Ile Asp Ala Ser
                20   25   30

Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys
        35   40   45

Thr Leu Lys Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala
    50   55   60

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Glu Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu
 65               70               75               80

Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro
             85               90               95

Glu Val Ile Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys
            100              105              110

Leu Val Ile Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Glu Ala
            115              120              125

Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn Asp
    130              135              140

Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe
145              150              155              160

Thr Val Thr Glu Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp
            165              170              175

Leu Asn Gly Ala Val Asp Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
            180              185              190

Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser
    195              200              205

Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val
    210              215              220

Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys
225              230              235              240

Pro Arg Ser Ser Ala Asp Arg Glu Ser Ile
             245              250
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